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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/086,464

DATE: 07/23/2002 8.6
TIME: 13:08:23

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\07232002\J086464.raw

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4 <110> APPLICANT: GORING, Daphne R. et al.
6 <120> TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
8 <130> FILE REFERENCE: P 25,762-A USA
10 <140> CURRENT APPLICATION NUMBER: US 10/086,464
11 <141> CURRENT FILING DATE: 2002-02-28
13 <150> PRIOR APPLICATION NUMBER: US 10/069,304
14 <151> PRIOR FILING DATE: 2002-02-19
16 <150> PRIOR APPLICATION NUMBER: PCT/CA00/00966
17 <151> PRIOR FILING DATE: 2000-08-18
19 <150> PRIOR APPLICATION NUMBER: US 60/149,466
20 <151> PRIOR FILING DATE: 1999-08-19
22 <150> PRIOR APPLICATION NUMBER: US 60/159,122
23 <151> PRIOR FILING DATE: 1999-10-13
25 <160> NUMBER OF SEQ ID NOS: 27
27 <170> SOFTWARE: PatentIn Ver. 2.1
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1944
31 <212> TYPE: DNA
32 <213> ORGANISM: Brassica napus
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (1)..(1944)
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40 Met Ser Ser Ala Pro Ser Pro Gly Thr Gly Ser Pro Pro Ser Pro Pro
41 1 5 10 15
43 tca aac tcc aca acc acc act cct cct cca gct tcc gct cct cct ccc 96
44 Ser Asn Ser Thr Thr Thr Pro Pro Pro Ala Ser Ala Pro Pro Pro
45 20 25 30
47 acc aca cct tct tct cct ccg ccg cca tcc act att ccg aca tct cct 144
48 Thr Thr Pro Ser Ser Pro Pro Pro Ser Thr Ile Pro Thr Ser Pro
49 35 40 45
51 cct cct tct tct cgc tct aca cct tct gct cct cct cca tct cca cca 192
52 Pro Pro Ser Ser Arg Ser Thr Pro Ser Ala Pro Pro Pro Ser Pro Pro
53 50 55 60
55 act cca tct acg ccg gga tct cca cct cct ctt cct cag ccg tct cca 240
56 Thr Pro Ser Thr Pro Gly Ser Pro Pro Pro Leu Pro Gln Pro Ser Pro
57 65 70 75 80
59 ccc gct cca act acg ccc gga tct cca ccc gca cct gtt act cct cct 288
60 Pro Ala Pro Thr Thr Pro Gly Ser Pro Pro Ala Pro Val Thr Pro Pro
61 85 90 95
63 act cga aac cct cca cct tca gtc cca gga cca ccg tcc aat cct tca 336
64 Thr Arg Asn Pro Pro Pro Ser Val Pro Gly Pro Pro Ser Asn Pro Ser

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65	100	105	110	
67 cgc gaa gga gga tct cct cga cct cca tct tct ccc tcg ccg ccg tct	384			
68 Arg Glu Gly Gly Ser Pro Arg Pro Pro Ser Ser Pro Ser Pro Pro Ser				
69 115 120 125				
71 cct tct tcc gac ggt tta tca aca gga gtg gtg gtg gga atc gcc atc	432			
72 Pro Ser Ser Asp Gly Leu Ser Thr Gly Val Val Val Gly Ile Ala Ile				
73 130 135 140				
75 gga gga gtc gct ctg ctt gtg ata gtg act ctg att tgt ctc ctc tgt	480			
76 Gly Gly Val Ala Leu Leu Val Ile Val Thr Leu Ile Cys Leu Leu Cys				
77 145 150 155 160				
79 aag aag aaa cga cgg aga gac gaa gaa gat gct tac tat gtt cct ccg	528			
80 Lys Lys Lys Arg Arg Arg Asp Glu Glu Asp Ala Tyr Tyr Val Pro Pro				
81 165 170 175				
83 cca cct cct cct ggt ccc aaa gcc gga gga cct tac ggt gga cag cag	576			
84 Pro Pro Pro Pro Gly Pro Lys Ala Gly Gly Pro Tyr Gly Gly Gln Gln				
85 180 185 190				
87 caa caa tgg cgg caa caa aac gca aca cca ccg tca gat cat gtc gtg	624			
88 Gln Gln Trp Arg Gln Gln Asn Ala Thr Pro Pro Ser Asp His Val Val				
89 195 200 205				
91 acg tca cta cca cca cca cct aag gct cca tct cca cca cgg caa cct	672			
92 Thr Ser Leu Pro Pro Pro Pro Lys Ala Pro Ser Pro Pro Arg Gln Pro				
93 210 215 220				
95 cct cca cct cca cca ccg cct ttc atg agc agc agc ggc ggc tcc gac	720			
96 Pro Pro Pro Pro Pro Pro Phe Met Ser Ser Ser Gly Gly Ser Asp				
97 225 230 235 240				
99 tac tcg gac cgt cca gtt ctt cct cca ccg tct cca ggg ctt gtg tta	768			
100 Tyr Ser Asp Arg Pro Val Leu Pro Pro Ser Pro Gly Leu Val Leu				
101 245 250 255				
103 ggc ttc tcc aaa agc act ttc aca tac gag gag cta gct aga gcc acc	816			
104 Gly Phe Ser Lys Ser Thr Phe Thr Tyr Glu Glu Leu Ala Arg Ala Thr				
105 260 265 270				
107 aat ggt ttc tcc gag gcg aac ttg tta gga caa ggc ggg ttc ggt tac	864			
108 Asn Gly Phe Ser Glu Ala Asn Leu Leu Gly Gln Gly Gly Phe Gly Tyr				
109 275 280 285				
111 gtg cac aaa ggt gtg ttg cct agt ggg aaa gaa gtt gct gtg aag cag	912			
112 Val His Lys Gly Val Leu Pro Ser Gly Lys Glu Val Ala Val Lys Gln				
113 290 295 300				
115 ttg aaa gtt ggg agt ggt cag gga gag agg gag ttt cag gca gag gtt	960			
116 Leu Lys Val Gly Ser Gly Gln Gly Glu Arg Glu Phe Gln Ala Glu Val				
117 305 310 315 320				
119 gag atc atc agc aga gtt cac cac agg cat ctg gtg tct ctt gtt ggt	1008			
120 Glu Ile Ile Ser Arg Val His His Arg His Leu Val Ser Leu Val Gly				
121 325 330 335				
123 tat tgc atc gcc ggt gcc aaa aga ttg ctt gtc tat gag ttt gtt cct	1056			
124 Tyr Cys Ile Ala Gly Ala Lys Arg Leu Leu Val Tyr Glu Phe Val Pro				
125 340 345 350				
127 aac aac aat ctc gag ctt cac ctc cat ggc gag gga cgg cct aca atg	1104			
128 Asn Asn Asn Leu Glu Leu His Leu His Gly Glu Gly Arg Pro Thr Met				
129 355 360 365				

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131 gaa tgg agc acc aga ttg aag att gct ctt gga tct gct aaa gga ctt 1152
132 Glu Trp Ser Thr Arg Leu Lys Ile Ala Leu Gly Ser Ala Lys Gly Leu
133      370      375      380
135 tct tat ctt cat gaa gat tgc aat cct aaa atc att cac cgt gat atc 1200
136 Ser Tyr Leu His Glu Asp Cys Asn Pro Lys Ile Ile His Arg Asp Ile
137 385      390      395      400
139 aag gct tca aac ata ttg ata gat ttc aag ttt gaa gct aag gtt gct 1248
140 Lys Ala Ser Asn Ile Leu Ile Asp Phe Lys Phe Glu Ala Lys Val Ala
141      405      410      415
143 gat ttt ggt ctt gct aag att gct tct gat aca aac acg cat gta tca 1296
144 Asp Phe Gly Leu Ala Lys Ile Ala Ser Asp Thr Asn Thr His Val Ser
145      420      425      430
147 aca cgt gtg atg gga acc ttt ggg tac ttg gct ccg gaa tac gct gca 1344
148 Thr Arg Val Met Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ala
149      435      440      445
151 agc gga aag ctc acg gag aag tct gac gtt ttc tca ttt ggc gtt gtg 1392
152 Ser Gly Lys Leu Thr Glu Lys Ser Asp Val Phe Ser Phe Gly Val Val
153      450      455      460
155 ctt ttg gag ctc att act gga cgt cga ccc gtt gat gcc aac aat gtc 1440
156 Leu Leu Glu Leu Ile Thr Gly Arg Arg Pro Val Asp Ala Asn Asn Val
157 465      470      475      480
159 tat gta gat gac agc tta gtt gac tgg gca cga cca ttg ctt aac cga 1488
160 Tyr Val Asp Asp Ser Leu Val Asp Trp Ala Arg Pro Leu Leu Asn Arg
161      485      490      495
163 gca tct gag caa gga gac ttt gag ggt tta gct gat gca aag atg aat 1536
164 Ala Ser Glu Gln Gly Asp Phe Glu Gly Leu Ala Asp Ala Lys Met Asn
165      500      505      510
167 aat ggg tat gac aga gag gag atg gct cgc atg gtt gct tgt gct gcg 1584
168 Asn Gly Tyr Asp Arg Glu Glu Met Ala Arg Met Val Ala Cys Ala Ala
169      515      520      525
171 gct tgt gtt cgc cat tca gct cgc cgc aga cct cgc atg agc cag att 1632
172 Ala Cys Val Arg His Ser Ala Arg Arg Arg Pro Arg Met Ser Gln Ile
173      530      535      540
175 gtg cgt gcg tta gaa gga aat gta tca ctg tca gat ctt aac gaa ggg 1680
176 Val Arg Ala Leu Glu Gly Asn Val Ser Leu Ser Asp Leu Asn Glu Gly
177 545      550      555      560
179 atg aga cca ggt caa agc aat gta tac agc tca tac gga gga agc acc 1728
180 Met Arg Pro Gly Gln Ser Asn Val Tyr Ser Ser Tyr Gly Gly Ser Thr
181      565      570      575
183 gat tat gac tcg agc cag tac aat gaa gac atg aag aag ttt agg aaa 1776
184 Asp Tyr Asp Ser Ser Gln Tyr Asn Glu Asp Met Lys Lys Phe Arg Lys
185      580      585      590
186 atg gca ctt gga act caa gag tac aac gcc acg ggt gag tac agt aat 1824
187 Met Ala Leu Gly Thr Gln Glu Tyr Asn Ala Thr Gly Glu Tyr Ser Asn
188      595      600      605
190 ccg acc agt gac tat gga ctg tac ccg tct ggt tca agc agc gag ggc 1872
191 Pro Thr Ser Asp Tyr Gly Leu Tyr Pro Ser Gly Ser Ser Ser Glu Gly
192      610      615      620
194 caa acc aca cgc gaa atg gag atg ggg aag att aag aga acc ggt cag 1920

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195 Gln Thr Thr Arg Glu Met Glu Met Gly Lys Ile Lys Arg Thr Gly Gln
196 625                      630                      635                      640
198 ggt tat agt gga cct tct ctt taa
199 Gly Tyr Ser Gly Pro Ser Leu
200                      645
203 <210> SEQ ID NO: 2
204 <211> LENGTH: 647
205 <212> TYPE: PRT
206 <213> ORGANISM: Brassica napus
208 <400> SEQUENCE: 2
209 Met Ser Ser Ala Pro Ser Pro Gly Thr Gly Ser Pro Pro Ser Pro Pro
210 1 5 10 15
211 Ser Asn Ser Thr Thr Thr Pro Pro Pro Ala Ser Ala Pro Pro Pro
212 20 25 30
213 Thr Thr Pro Ser Ser Pro Pro Pro Pro Ser Thr Ile Pro Thr Ser Pro
214 35 40 45
215 Pro Pro Ser Ser Arg Ser Thr Pro Ser Ala Pro Pro Pro Ser Pro Pro
216 50 55 60
217 Thr Pro Ser Thr Pro Gly Ser Pro Pro Pro Leu Pro Gln Pro Ser Pro
218 65 70 75 80
219 Pro Ala Pro Thr Thr Pro Gly Ser Pro Pro Ala Pro Val Thr Pro Pro
220 85 90 95
221 Thr Arg Asn Pro Pro Pro Ser Val Pro Gly Pro Pro Ser Asn Pro Ser
222 100 105 110
223 Arg Glu Gly Gly Ser Pro Arg Pro Pro Ser Ser Pro Ser Pro Pro Ser
224 115 120 125
225 Pro Ser Ser Asp Gly Leu Ser Thr Gly Val Val Val Gly Ile Ala Ile
226 130 135 140
227 Gly Gly Val Ala Leu Leu Val Ile Val Thr Leu Ile Cys Leu Leu Cys
228 145 150 155 160
229 Lys Lys Lys Arg Arg Arg Asp Glu Glu Asp Ala Tyr Tyr Val Pro Pro
230 165 170 175
231 Pro Pro Pro Pro Gly Pro Lys Ala Gly Gly Pro Tyr Gly Gly Gln Gln
232 180 185 190
233 Gln Gln Trp Arg Gln Gln Asn Ala Thr Pro Pro Ser Asp His Val Val
234 195 200 205
235 Thr Ser Leu Pro Pro Pro Pro Lys Ala Pro Ser Pro Pro Arg Gln Pro
236 210 215 220
237 Pro Pro Pro Pro Pro Pro Pro Phe Met Ser Ser Ser Gly Gly Ser Asp
238 225 230 235 240
239 Tyr Ser Asp Arg Pro Val Leu Pro Pro Pro Ser Pro Gly Leu Val Leu
240 245 250 255
241 Gly Phe Ser Lys Ser Thr Phe Thr Tyr Glu Glu Leu Ala Arg Ala Thr
242 260 265 270
243 Asn Gly Phe Ser Glu Ala Asn Leu Leu Gly Gln Gly Gly Phe Gly Tyr
244 275 280 285
245 Val His Lys Gly Val Leu Pro Ser Gly Lys Glu Val Ala Val Lys Gln
246 290 295 300
247 Leu Lys Val Gly Ser Gly Gln Gly Glu Arg Glu Phe Gln Ala Glu Val

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```

248 305          310          315          320
249 Glu Ile Ile Ser Arg Val His His Arg His Leu Val Ser Leu Val Gly
250          325          330          335
251 Tyr Cys Ile Ala Gly Ala Lys Arg Leu Leu Val Tyr Glu Phe Val Pro
252          340          345          350
253 Asn Asn Asn Leu Glu Leu His Leu His Gly Glu Gly Arg Pro Thr Met
254          355          360          365
255 Glu Trp Ser Thr Arg Leu Lys Ile Ala Leu Gly Ser Ala Lys Gly Leu
256          370          375          380
257 Ser Tyr Leu His Glu Asp Cys Asn Pro Lys Ile Ile His Arg Asp Ile
258 385          390          395          400
259 Lys Ala Ser Asn Ile Leu Ile Asp Phe Lys Phe Glu Ala Lys Val Ala
260          405          410          415
261 Asp Phe Gly Leu Ala Lys Ile Ala Ser Asp Thr Asn Thr His Val Ser
262          420          425          430
263 Thr Arg Val Met Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ala
264          435          440          445
265 Ser Gly Lys Leu Thr Glu Lys Ser Asp Val Phe Ser Phe Gly Val Val
266          450          455          460
267 Leu Leu Glu Leu Ile Thr Gly Arg Arg Pro Val Asp Ala Asn Asn Val
268 465          470          475          480
269 Tyr Val Asp Asp Ser Leu Val Asp Trp Ala Arg Pro Leu Leu Asn Arg
270          485          490          495
271 Ala Ser Glu Gln Gly Asp Phe Glu Gly Leu Ala Asp Ala Lys Met Asn
272          500          505          510
273 Asn Gly Tyr Asp Arg Glu Glu Met Ala Arg Met Val Ala Cys Ala Ala
274          515          520          525
275 Ala Cys Val Arg His Ser Ala Arg Arg Arg Pro Arg Met Ser Gln Ile
276          530          535          540
277 Val Arg Ala Leu Glu Gly Asn Val Ser Leu Ser Asp Leu Asn Glu Gly
278 545          550          555          560
279 Met Arg Pro Gly Gln Ser Asn Val Tyr Ser Ser Tyr Gly Gly Ser Thr
280          565          570          575
281 Asp Tyr Asp Ser Ser Gln Tyr Asn Glu Asp Met Lys Lys Phe Arg Lys
282          580          585          590
283 Met Ala Leu Gly Thr Gln Glu Tyr Asn Ala Thr Gly Glu Tyr Ser Asn
284          595          600          605
285 Pro Thr Ser Asp Tyr Gly Leu Tyr Pro Ser Gly Ser Ser Ser Glu Gly
286          610          615          620
287 Gln Thr Thr Arg Glu Met Glu Met Gly Lys Ile Lys Arg Thr Gly Gln
288 625          630          635          640
289 Gly Tyr Ser Gly Pro Ser Leu
290          645
293 <210> SEQ ID NO: 3
294 <211> LENGTH: 2189
295 <212> TYPE: DNA
296 <213> ORGANISM: Brassica napus
300 <220> FEATURE:
301 <221> NAME/KEY: CDS

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/086,464

DATE: 07/23/2002
TIME: 13:08:24

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\07232002\J086464.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 3,12,15,18,21,22,25
Seq#:19; Xaa Pos. 7
Seq#:20; N Pos. 3,6,8,9,15,18,21,22
Seq#:23; N Pos. 2,3,5,6,9,12,14,15,18,21

VERIFICATION SUMMARY

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L:310 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 3, CDS LOCATION:1..2189
L:2086 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:2100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:2118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:2158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0